

**REMARKS**

In the specification:

The title and the abstract have been replaced to address the issues of the Examiner.

In the claims:

**Claim Rejections Under 35 U.S.C. 101/112, first paragraph.**

The Examiner has rejected claims 1-13 under 35 U.S.C. 101 or 112, first paragraph, because the claimed invention is not supported by either a specific and substantial asserted utility or a well-established utility.

According to the amended claims, Applicants have identified MYB domain transcription factors that are expressed when plant cells are exposed to a pathogen. The transcription factors were identified as MYB domain transcription factors after a careful sequence analysis of the genes and identifying the characteristic MYB domain in the sequences. Additionally, Applicants have established that when some of the identified transcription factors are overexpressed in a plant the plant had an improved phenotype for plant disease/pathogen tolerance.

Thus, Applicants believe that a sufficient specific and substantial asserted utility is established by the present invention. It is well-known that to trigger disease or pathogen resistance in a plant the expression of specific genes is necessary. It would make sense that additionally it would be required to increase the levels of specific transcription factors to achieve that purpose. Applicants have identified such transcription factors. It makes sense that if a transcription factor (containing the characteristic MYB domain) is preferentially expressed under specific conditions, such as when exposed to a pathogen, that overexpression of the transcription factor in a plant will lead to increased pathogen tolerance

In view of the amended claims and remarks, Applicants respectfully submit that the claims overcome the Examiner's rejections and that the claims are in condition for allowance.

**Claim Rejections Under 35 U.S.C. 101/112, second paragraph.**

The Examiner has rejected claims 1,2, 5, 6, 9, 10 and 13 under 35 U.S.C. 112, second paragraph, as being indefinite for being in improper Markush format. The amended claims include the appropriate correction.

The Examiner has rejected claims 2, 6, and 10 under 35 U.S.C. 112, second paragraph, in that the phrase "conserved domain" is indefinite.

Applicants have amended the claims to particularly point out what conserved domains are envisioned from Figure 1.

At claims 4 and 8, Applicants have amended the claims to --tissue-preferred--. At claims 5, 9 and 13, Applicants have deleted the selection step as suggested by the Examiner.

At claims 5 and 13, the Examiner states the term "altering" is indefinite. However the specification at pages 6 and 7 provides a thorough list of what altering or modifying entails. Gene expression levels in a transgenic plant can be modified to the extent of 5%, 10%, 70%, 100% compared with a nontransgenic plant. The same is true with respect to a characteristic associated with disease resistance or tolerance as provided at page 7. Therefore, Applicants believe that the term "altering" is definite.

At claim 9, the term gene refers to any gene in a cell and is not restricted to the polynucleotides of the invention.

Thus, Applicants respectfully submit that the new claims and remarks overcome the Examiner's rejections and that the claims are in condition for allowance.

#### **Claim Rejections Under 35 U.S.C. 102(e).**

The Examiner has rejected claims 1-13 under 35 U.S.C. 102(e) as being anticipated by Klessig et al.

The Yamaguchi-Shinozaki reference teaches an isolated nucleic acid molecule which encodes a myb homologue involved in the regulation of disease. However, the reference does not provide the sequences of the present invention. Therefore, the reference fails to anticipate the present invention.

Applicants respectfully submit that the new claims and remarks overcome the Examiner's rejections and that the claims are in condition for allowance.

#### **Provisional Double Patenting Rejection.**

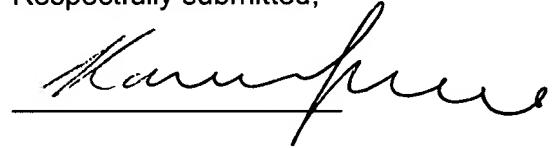
The Examiner has rejected claims 1-14 under the judicially created obviousness-type double patenting doctrine over claims in copending application Ser. No. 09/532,591.

In view of the new claims and remarks, applicants respectfully submit that the claims as now written overcome the Examiner's rejections and that the claims are in condition for allowance.

Please charge deposit account 501025 a one month extension of time.

Please direct all telephone calls to Karen J. Guerrero at 510-264-0280.

Respectfully submitted,



Karen Guerrero  
Reg. No. 37,071

Date: March 26, 2001

Mendel Biotechnology, Inc  
21375 Cabot Blvd  
Hayward, CA 94545

**VERSION WITH MARKINGS TO SHOW CHANGES MADE**

1. (Once amended) A transgenic plant comprising a recombinant polynucleotide comprising a nucleotide sequence encoding a polypeptide comprising at least 6 consecutive amino acids of a sequence selected from the group consisting of SEQ ID Nos. [2N, where N=1-56] 32, 40, 58, 62, 68, 86, 88, 94, and 112, wherein the recombinant polynucleotide alters the plant's disease tolerance or resistance when compared with the same trait of another plant lacking the recombinant polynucleotide.
2. (Once Amended) The transgenic plant of claim 1, wherein the nucleotide sequence encodes a polypeptide comprising a conserved domain selected from the group consisting of conserved domains provided in Figure 1 for SEQ ID Nos. [2N, where N=1-56] 32, 40, 58, 62, 68, 86, 88, 94, and 112.
3. The transgenic plant of claim 1, wherein the recombinant polynucleotide further comprises a promoter operably linked to said nucleotide sequence.
4. (Once Amended) The transgenic plant of claim 3, wherein said promoter is constitutive or inducible or [tissue-active] tissue-preferred.
5. (Once Amended) A method for altering the disease tolerance or resistance of a plant, said method comprising (a) transforming a plant with a recombinant polynucleotide comprising a nucleotide sequence encoding a polypeptide comprising at least 6 consecutive amino acids of a sequence selected from the group consisting of SEQ ID Nos. [2N, where N=1-56] 32, 40, 58, 62, 68, 86, 88, 94, and 112, [(b) selecting said transformed plants]; and [(c)] (b) identifying a transformed plant having an altered disease tolerance or resistance.
6. (Once Amended) The method of claim 5, wherein the nucleotide sequence encodes a polypeptide comprising a conserved domain selected from the group consisting of conserved domains provided in Figure 1 for SEQ ID Nos. [2N, where N=1-56] 32, 40, 58, 62, 68, 86, 88, 94, and 112.
7. The method of claim 5, wherein the recombinant polynucleotide further comprises a promoter operably linked to said nucleotide sequence.
8. (Once Amended) The method of claim [7] 8, wherein said promoter is constitutive or inducible or [tissue-active] tissue-preferred.
9. (Once Amended) A method for altering the expression levels of at least one gene in a plant, said method comprising (a) transforming the plant with a recombinant polynucleotide comprising a nucleotide sequence encoding a polypeptide comprising at least 6 consecutive amino acids of a sequence selected from the group consisting of SEQ ID Nos. [2N, where N=1-56] 32, 40, 58, 62, 68, 86, 88, 94, and 112; and (b)

[selecting said transformed plant] identifying a transformed plant having an altered disease tolerance or resistance.

10. (Once Amended) The method of claim [10] 9, wherein said recombinant polynucleotide encodes a polypeptide comprising a conserved domain selected from the group consisting of conserved domains provided in Figure 1 for SEQ ID Nos. [2N, where N=1-56] 32, 40, 58, 62, 68, 86, 88, 94, and 112.

11. (Once Amended) The method of claim [10] 9, wherein the nucleotide sequence further comprises a promoter operably linked to said nucleotide sequence.

12. (Once Amended) The method of claim [10] 9, wherein said promoter is constitutive or inducible or tissue-[active] preferred.

13. (Once Amended) A method for altering the disease tolerance or resistance in a plant, said method comprising (a) transforming the plant with a recombinant polynucleotide comprising at least 18 consecutive nucleotides of a sequence selected from the group consisting of SEQ ID Nos. [2N-1, where N= 1-56, and SEQ ID Nos. 113-121] 31, 39, 57, 61, 67, 85, 87, 93, 111 and 120; and (b) [selecting said transformed plant] identifying a transformed plant having an altered disease tolerance or resistance.